



Development of a breeding program for improving the milk yield performance of Butana cattle under smallholder production conditions using a stochastic simulation approach

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ABSTRACT

Butana is one of the local dairy cattle breeds of Sudan commonly kept by smallholder producers. This breed has been strongly promoted to advance the dairy production sector in the country. The main problem, however, is the lack of a systematic breeding program that involves smallholder producers. The aim of the current study was to identify the most promising design for a breeding program to improve the milk yield performance of Butana cattle under smallholder production conditions. In total, 3 breeding scenarios, including (1) the use of farm bulls, (2) the use of village bulls, and (3) the rotational use of village bulls within village groups, were simulated using a stochastic simulation approach. For each breeding scenario, 3 selection methods for bulls were considered, namely random mating, phenotypic selection, and selection based on estimated breeding value (EBV). The results showed that no genetic gain was realized with random mating in all breeding scenarios. In the farm bull breeding scenario, annual genetic gain (standard deviation units) ranged from 0.01 to 0.19 (phenotypic selection) and from 0.01 to 0.39 (selection based on EBV). In the village bull breeding scenarios, the annual genetic gain ranged from 0.01 to 0.21 (phenotypic selection) and 0.01 to 0.45 (selection based on EBV). The lowest genetic gain was realized for the rotational use of village bulls among villages within groups. Through the rotational use of village bulls, however, a higher genetic variance was maintained than in the farm and village bull breeding scenarios. We concluded that a village bull breeding program with selection based on EBV of young bulls was the most promising breeding design for achieving

the breeding goal. Further studies are needed to assess the organizational feasibility of such a breeding program to ensure the participation of smallholder producers and its sustainability.

Key words: Butana cattle, breeding program

INTRODUCTION

In Sudan, indigenous cattle are managed by smallholder producers and traditional pastoralists. They play an essential role in the Sudanese economy and are considered a major component of poverty alleviation initiatives (Wilson, 2018). Among Sudanese indigenous cattle, Butana is one of the most promising breeds suited for milk production due to its comparatively high production performance. The breed produces around 1,663 kg of milk per lactation under research station management conditions (Musa et al., 2005). It is predominantly kept by semi-nomadic pastoralists under smallholder production conditions in the Butana region of central Sudan. The breed is well adapted to the harsh environment and poor nutritional conditions of this semi-arid region (Ahmed et al., 2017). Within-breed selection is practiced on a research station to genetically improve the milk yield performance of the breed. However, Butana cattle farmers are not actively involved in the planning and implementation of this public breed improvement program (Omer et al., 2020), and they often do not have access to the improved genetics. Therefore, many Butana cattle farmers are more focused on crossbreeding with Holstein Friesian cattle (Musa et al., 2005; Ahmed et al., 2007) as a method to quickly improve the milk yield and their income from milk sales (Abdel Gader et al., 2007; Omer et al., 2020). However, the extensive and unsystematic crossbreeding of Butana with Holstein Friesian has raised concerns over the fate and conservation of the Butana breed for present and future use (Musa et al., 2005). This points to the need for simple and effective breeding programs that actively involve smallholder farmers and optimize genetic gain for milk yield while maintaining the breed's

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adaptation to smallholder production conditions. Co-operative village breeding programs have been widely suggested as an alternative option to central breeding schemes (Kahi et al., 2005; Wurzinger et al., 2008; Rewe et al., 2009). They constitute a means to overcome the constraints associated with managing a breed improvement program for smallholder herds, namely small herd sizes, low levels of organization and infrastructure, and lack of performance recording and animal identification (Rege et al., 2011). In addition, cooperative breeding programs are considered appropriate for the conservation of indigenous livestock breeds and can contribute significantly to livestock genetic improvement in developing countries (Gizaw et al., 2009, 2014; Mueller et al., 2015). The design of livestock breeding programs implies proper breeding planning and evaluation of alternative breeding scenarios to identify the most appropriate breeding scheme. Therefore, the objective of the present study was to compare alternative breeding and selection scenarios of a cooperative village breeding program for the genetic improvement of the milk yield performance of Butana cattle through a simulation study.

MATERIALS AND METHODS

The simulation of alternative breeding and selection scenarios was performed using AlphaSimR (Gaynor et al., 2019) within R software version 3.6.3 (<https://www.r-project.org/>). Use of AlphaSimR involved a 2-step approach including a burn-in phase described as historic breeding and an evaluation phase called future breeding. The simulation was specifically designed to mimic the real Butana cattle population in central Sudan. No animals were used in this study, and ethical approval for the use of animals was thus deemed unnecessary.

Burn-in Phase

The haplotype sequences of a founder population consisting of 5,000 animals were simulated via a Markovian Coalescent Simulator (Chen et al., 2009) using the runMacs2 function of AlphaSimR (Gaynor et al., 2019). The parameters used for creating the founder haplotypes included effective population sizes (N_e) over many generations, which describe the demographic history of cattle populations [MacLeod et al., 2013; i.e., $N_e = 6,000$ animals (1,000 generations ago), $N_e = 24,000$ animals (10,000 generations ago), and $N_e = 48,000$ animals (100,000 generations ago)]. The N_e in the current generation was set to 1,035 animals, which reflected the high genetic diversity found in cattle populations in Africa (Powell et al., 2019). The founder genotypes were simulated with 10 chromosome pairs,

each with 10^8 base pairs length, mutation rate of 1×10^{-8} per base pair per generation, and 5,000 randomly chosen SNP marker loci. In addition, 1,000 QTL per chromosome was considered to be the causal loci of a polygenic trait influenced by many genes, each of them with minor effects. The chosen number of QTL per chromosome is consistent with many published studies (e.g., Obsteter et al., 2019, 2021; Selle et al., 2020). The simulated haplotypes were used to establish the founder population of 5,000 animals with 1:1 sex ratio. The sex of founder animals was randomly assigned.

A single polygenic trait was modeled with a pure additive genetic effect, and the initial mean genetic value and genetic variance for the trait were set to 0 and 1, respectively. Furthermore, QTL allele substitution effects were sampled from a standard normal distribution, and for each animal, the true breeding value (TBV) for the simulated trait was calculated by adding up its coded genetic value for its genotype across all QTLs. A narrow-sense heritability of 0.35 was assumed, and the phenotype (y_i) for each animal was simulated by adding a random residual environmental effect (random error) to each animal's TBV. Thus, $y_i = g_i + e_i$, where g_i denotes TBV of animal i , and e_i is the random error effect, which was drawn from a normal distribution with a mean of zero and a variance equals to the residual variance.

In the current simulation, we chose 1 polygenic trait to reflect the farmers' production trait preferences for future genetic improvement in Butana cattle as determined by a survey in a previous study (Omer et al., 2020).

Evaluation Phase

In the evaluation phase, initial parents (first generation) of the breeding program consisted of 1,650 cows and 202 bulls randomly selected from the founder population. Three different breeding scenarios were simulated over 10 generations across where the number of cows remained constant. In each scenario, animals were randomly assigned to 202 farms in 17 villages according to their predefined herd size that varied from 2 to 23 cows (Table 1). These numbers represented the real number of villages, Butana cattle herds, and cows in the Butana region of Sudan (Omer et al., 2020). The 3 different breeding scenarios are hereby described.

Farm Bull Breeding Scenario

In the farm bull breeding scenario, it was assumed that each farm used its own breeding bull to improve the milk yield. The initial farm bulls ($n = 202$) were randomly selected from the founder population, and 1

Table 1. Number of farms and cows used for breeding program simulation

Village	Farms (no.)	Cows (no.)	Average number of cows per farm
1	23	276	12
2	6	48	8
3	28	168	6
4	19	76	4
5	13	65	5
6	10	40	4
7	4	36	9
8	11	66	6
9	2	8	4
10	5	10	2
11	11	55	5
12	23	460	20
13	4	92	23
14	3	24	8
15	6	66	11
16	22	88	4
17	12	72	6
Total	202	1,650	8

bull was randomly assigned to each farm. The decision to assign a breeding bull to each farm, including those with small herd sizes, was motivated by the observation that some Butana cattle farmers tend to keep breeding bulls within small-sized herds of up to 2 cows (Omer et al., 2020). For farmers with small herd sizes, however, this could be costly and could affect the economic viability of the scheme. In this breeding scenario, the selection of young bulls was carried out within each farm.

Village Bull Breeding Scenario

The village bull breeding scenario assumed a cooperation between farms in the same village, meaning that all farms in one village used the same bull to mate their cows. For the 17 villages assumed, average number of farms per village ranged from 2 to 28, and the number of cows per village varied from 8 to 460 animals (Table 1). The required village breeding bulls ($n = 17$) were randomly selected from the list of farm bulls ($n = 202$), and 1 bull was assigned to each village.

Rotational Use of Village Bulls Within Village Groups Scenario

The rotational use of village bulls within village groups assumed a cooperation among villages within the same administrative unit. Based on the distribution of administrative units, the 17 villages were further combined into 5 groups. The number of cooperative villages within a group ranged from 1 to 6 (Table 2), with

12 to 80 farms and 72 to 730 cows each. Rotation of the village bulls among villages within the same group was assumed, meaning that after a breeding cycle of about a year, a village's bull was transferred to another village in the same group. As groups 1 and 5 had only 1 village each, rotation was not possible in these groups, hence their exclusion from subsequent analyses.

Both village bull breeding scenarios were used to create genetic relationships between the herds. For all breeding scenarios, 3 alternative selection methods for breeding bulls were considered. These included (1) random mating, in which bulls were randomly selected to mimic the situation where farmers use bulls based on availability rather than genetic merit, (2) phenotypic selection (phenotypic observations on the individual itself), and (3) selection based on EBV for the breeding goal trait. Here, we assumed that farmers keep performance records of cow's milk yield, and that the bulls are evaluated and selected based on their relatives' performances. Thus, EBV of bulls were computed from all available phenotype information from a bull's relatives using a standard mixed model.

In the 2-village bull breeding scenarios, selection of young bulls was carried out within the respective village or group. No selection on the female path was assumed, meaning that all female calves were used for further breeding, replacing the respective number of old cows in each farm, regardless of their genetic merit.

For each breeding scenario and selection method, the mean genetic gain and variance were extracted into a csv file. The genetic gain in each generation was expressed in units of standard deviation (SD units) of the TBV, whereas the genetic variance is the variance of the breeding value (additive genetic variance, V_A). Furthermore, annual genetic gain was estimated by dividing the genetic gain per generation by the generation interval from the bull side. A generation interval of 5 yr was assumed for bulls used in the farm and village bull breeding scenarios, considering the age of bull at first mating and reproductive lifetime of bulls to be 2 and 3 yr, respectively. Generation interval differed for the rotational use of village bulls within groups scenario.

Table 2. Number of cooperative groups, farms, and cows per group used for breeding program simulation

Group	Cooperative villages (no.)	Farms per group (no.)	Cows per group (no.)
1	1	23	276
2	6	80	433
3	4	29	139
4	5	58	730
5	1	12	72

Due to additional time required to complete the rotation within a group, generation interval was assumed to be 6 yr for group 3, which consisted of 4 cooperative villages; 7 yr for group 4 with 5 cooperative villages; and 8 yr for group 2 with 6 cooperative villages.

Data Analysis

The results were graphically visualized using R software version 3.6.3. For each breeding scenario, the genetic gains and genetic variances over the generation under the 3 selection methods were presented as line charts. Comparisons of genetic gains and genetic variances under the 3 breeding scenarios with different selection methods were presented as bar charts. Tukey's test for pairwise comparisons under a 2-way ANOVA model was performed to detect significant ($P < 0.05$) differences in annual genetic gain and variance within and between the breeding scenarios and selection methods.

RESULTS

Genetic Trends of the Breeding Scenarios and Selection Methods

Genetic gain and variance in the simulated trait for random mating, phenotypic selection, and selection based on EBV in the farm bull breeding scenario through the period of 10 generations are presented in Figures 1A and 1B, respectively. Notably, with random mating, almost no genetic gain was realized, whereas the genetic gain gradually increased with phenotypic selection and selection based on EBV over each generation. Compared with phenotypic selection, the genetic gain achieved by selection based on EBV was approximately doubled after the tenth generation (Figure 1A). As shown in Figure 1B, the genetic variance decreased as the number of generations increased, irrespective of the selection method. Across generations, the genetic variance was comparatively higher with selection based on EBV than with phenotypic selection or random mating.

Similar to the farm bull breeding scenario, approximately no genetic gain was realized when village bulls were randomly mated, whereas a positive genetic trend was observed when phenotypic selection and selection based on EBV selection of village bulls were applied (Figure 2A). Again, the genetic gain was generally higher for selection based on EBV than that for phenotypic selection of village bulls. Consequently, only 6 generations of selection are needed with selection based on EBV to achieve the same genetic gain (0.21 SD) as

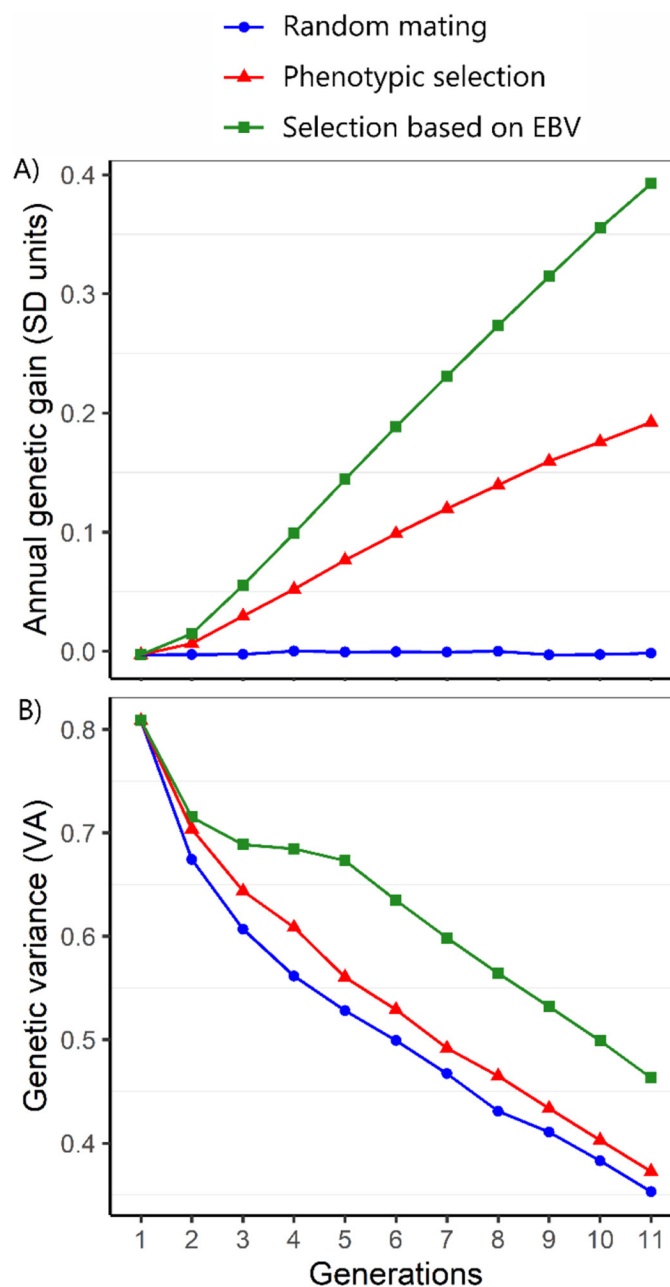


Figure 1. Annual genetic gain (A) and genetic variance (B) over 10 generations of selection under the farm bull breeding scenario.

with phenotypic selection after 10 generations. Under the village bull breeding scenario, the genetic variance decreased throughout the generations, irrespective of the selection method (Figure 2B).

Figures 3A and 3B show the genetic gains and genetic variances for the rotational use of village bulls within village groups. For phenotypic and selection based on EBV, the genetic gain considerably fluctuated between

generations 2 and 6, and subsequently increased after generation 7. Generally, the highest genetic gain was realized using selection based on EBV (Figure 3A). For all 3 selection methods, the genetic variance decreased between generations 2 and 6, whereas it fluctuated for phenotypic selection and selection based on EBV, and increased for random mating after generation 7 (Figure 3B).

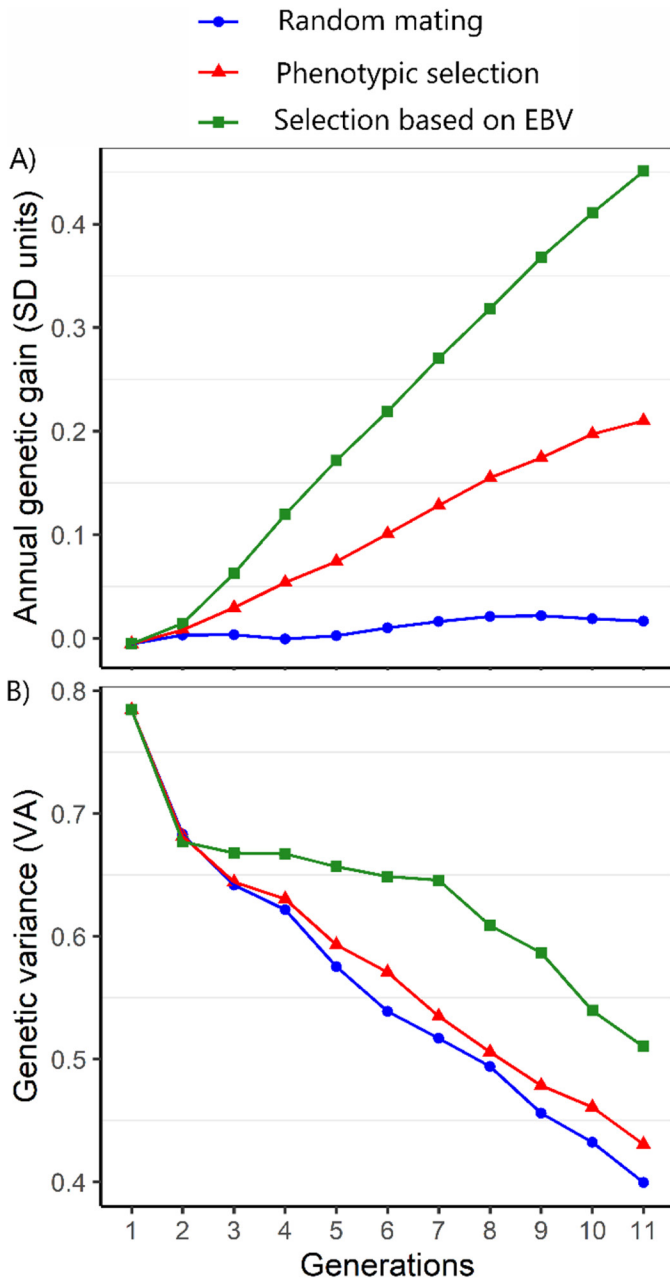


Figure 2. Annual genetic gain (A) and genetic variance (B) over 10 generations of selection under the village bull breeding scenario.

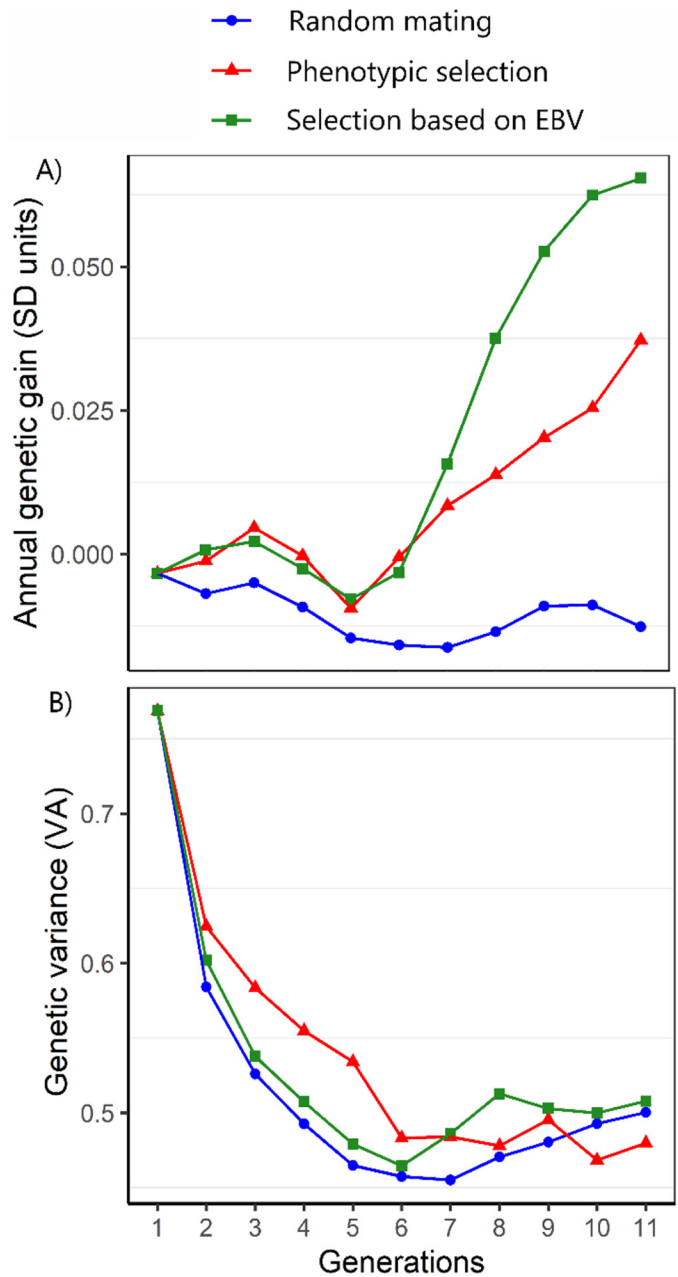


Figure 3. Annual genetic gain (A) and genetic variance (B) over 10 generations of selection under the rotational use of village bulls within village groups scenario.

Genetic Gain and Genetic Variance After 10 Generations of Selection

Comparisons of both genetic gain and variance for the simulated trait were made between the 3 breeding scenarios and selection methods after 10 generations as shown in Figures 4 and 5. With selection based on EBV, differences in genetic gain across breeding scenarios were significant at $P < 0.001$ (Figure 4). The

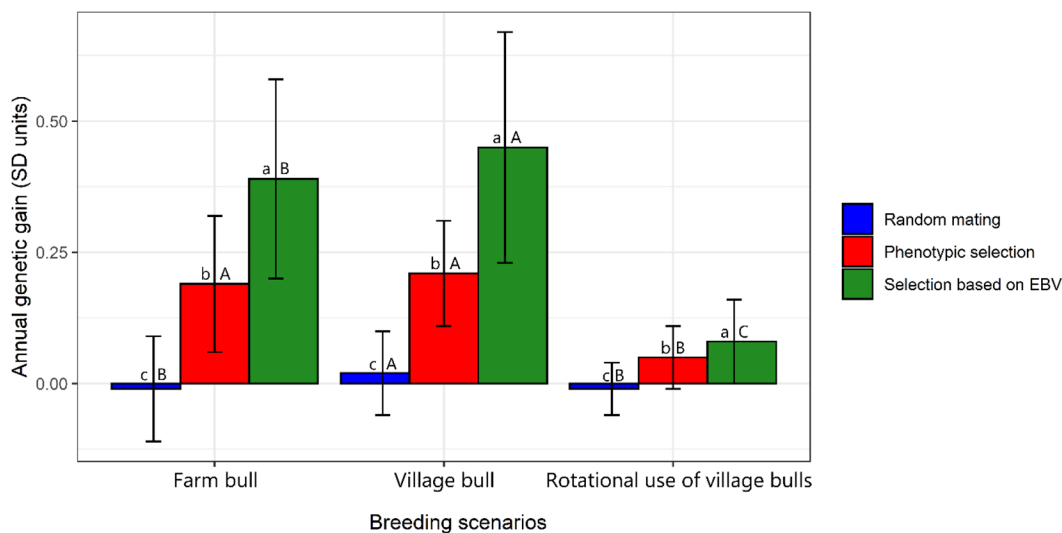


Figure 4. Annual genetic gain across all breeding scenarios after 10 generations of selection. Capital letters (A–C) indicate differences between the breeding scenarios within each selection method ($P < 0.05$) and lowercase letters (a–c) indicate differences between the selection methods within the same breeding scenario. Error bars indicate SD.

village bull breeding scenario resulted in the highest annual genetic gain (0.45 ± 0.22 SD), whereas the lowest was found for rotational use of village bulls within village groups (0.07 ± 0.07 SD). The rotational use of village bulls with phenotypic selection also yielded significantly ($P < 0.001$) lower genetic gains compared with the same selection method under the farm bull or village bull breeding scenario. Both the farm bull breeding scenario and the rotational use of village bulls had a negative genetic gain with random selection of

bulls. When evaluating the genetic variance after 10 generations of breeding, the rotational use of village bulls within village groups retained significantly higher genetic variance with random mating and phenotypic selection compared with the farm bull and village bull breeding scenarios with the same selection methods ($P < 0.001$; Figure 5). However, genetic variances for the village bull breeding scenario were significantly higher than those of the farm bull breeding scenario across all 3 methods of selection ($P < 0.05$).

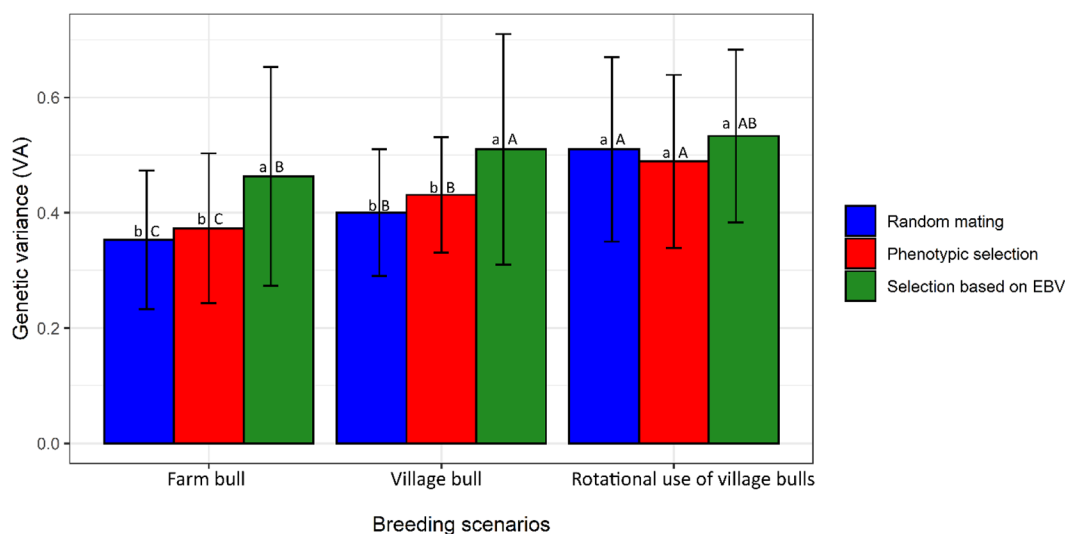


Figure 5. Genetic variance across all breeding scenarios after 10 generations of selection. Capital letters (A–C) indicate differences between the breeding scenarios within each selection method ($P < 0.05$) and lowercase letters (a,b) indicate differences between the selection methods within the same breeding scenario. Error bars indicate SD.

DISCUSSION

A breeding program based on within-breed selection has been advocated as a way of developing Butana cattle, which are predominantly found in marginal habitats and harsh environments. Previous studies investigated the possibility of developing of a community-based breeding program for the genetic improvement of Butana cattle through a survey approach (Omer et al., 2020). Following that investigation, the present study simulated 3 alternative breeding scenarios, including a farm bull, a village bull, and the rotational use of village bulls within village groups using different methods of bull selection, namely random mating, phenotypic selection, and selection based on EBV, to identify the most promising breeding program for the genetic improvement of this breed. Genetic gain in the simulated trait was used to compare the alternative breeding scenarios and selection methods. Our results showed a relatively high genetic gain for the simulated trait under all selection methods of the village bull breeding scenario. This could be attributed to a high selection intensity in this scenario as fewer number of bulls were needed. Thus, farmers collaborated in each village, and their herds were considered as 1 selection group from which a bull was chosen. According to Powell et al. (2019) and Selle et al. (2020), the genetic connectedness between herds improves the accuracy of selected parents, thus resulting in higher genetic improvement. Similarly, village breeding programs have been suggested for genetic improvement of different breeding goal traits for indigenous livestock species in the tropics. For instance, a village breeding program has been implemented to improve pure Lobi cattle and their crosses (Lobi × Zebu) for meat production and trypanotolerance in southwest of Burkina Faso (Ouédraogo et al., 2021). In India, a village breeding program has been implemented to conserve the Tharparkar cattle breed (FAO, 2013). In this breeding program, Tharparkar bulls were selected, and each bull was given to a family in the village who agreed to maintain it in exchange for earnings obtained through the use of the bull by other farmers for natural service mating of their cows. The breeding program has shown an increase of the number of pure Tharparkar cows. In addition, a village-based breeding program was suggested for improving beef production of indigenous cattle in the Mangwe district of Zimbabwe (Bidi et al., 2015). In small ruminants, several studies have shown that village breeding programs yield acceptable genetic improvement, for example, a cooperative village breeding program for Menz, Bonga, and Horro sheep and for western lowland and Abergelle goats for smallholder farming systems in Ethiopia (Gizaw et al., 2009; Abegaz et al., 2014; Haile et al., 2020). Similarly, a

village-based breeding program for an llama population in Bolivia has been suggested to improve fiber production (Wurzinger et al., 2008).

Our present simulation confirmed the benefits of cooperative breeding programs and demonstrated the potential of a village bull breeding program for future improvement of Butana herds under smallholder production conditions. Nevertheless, from a practical perspective, its implementation requires the involvement of farmers who are willing to genetically improve their cattle and to take an active part in the development and implementation of any measure from the design to the implementation phase (van Arendonk, 2011; Mueller et al., 2015; Haile et al., 2020). The willingness of Butana cattle farmers to engage in associations and exchange information (Omer, et al., 2020) could aid the design and practical implementation of a village bull breeding program for Butana cattle. Furthermore, a village bull breeding program may only require a minimal change in already existing breeding methods among farmers, because some Butana cattle farmers already rely on bulls from their neighbors (Musa et al., 2006; Omer et al., 2020). The village bull breeding program simulated in the present study only assumed a single bull mating to all village herds. However, for better use of a bull within village herds, where possible, the development of village-run AI schemes using frozen or fresh semen (Rege et al., 2011; van Arendonk, 2011) could be considered as a complement or alternative method to the natural bull mating. Use of AI to exchange genetic material between village herds offers an opportunity to further increase the rate of genetic improvement (van Arendonk, 2011).

In contrast to the village bull breeding scenario, lower genetic gains achieved with the farm bull breeding scenario in the present study indicated that genetic progress by individual efforts of farmers is difficult because of small herd sizes. In addition, the high loss in genetic variance under the farm bull breeding scenario was most likely due to inbreeding and the continuous selection of farm bulls within a farm herd (Gorjanc et al., 2015). However, the genetic variance is considered a key factor for genetic improvement, control of inbreeding, and effective utilization and exploitation of breed-specific characteristics (Makina et al., 2014; Cervantes et al., 2016; Ouédraogo et al., 2021). Generally, in a sustainable breeding program, sufficient rates of genetic gain in the short term, and the maintenance of genetic variance in the long term, have to be considered (Bijma et al., 2001).

Several types of rotational mating systems exist, but in general, males that are used as sires are provided from another subpopulation than dams (Windig and Kaal, 2008). This type of rotational mating was

evaluated in the present study. The results showed that across all selection methods, the rotational mating achieved lower genetic gain than the village bull breeding scenario. This could be attributed to the low number of selection cycles for bulls in the simulated rotational breeding scenario because, on average, bulls were rotated 4 to 6 yr before selection of young bulls was carried out to replace the old ones. This implied a longer generation interval for bulls in the rotational breeding scenario as compared with both the village and farm bull breeding scenarios. Conversely, shortening of generation intervals will result in more rounds of selection per unit time, hence increasing the achievable gains per unit time (Kariuki et al., 2014; Kasinathan et al., 2015). However, one positive aspect of the rotational use of village bulls within village groups is that a higher genetic variance can be maintained. Our results support previous findings that rotational mating can be generally used to increase the genetic diversity within a breed by balancing the genetic contributions of the breed's subpopulations (Windig and Kaal, 2008; Mucha and Komen, 2016). Therefore, in situations where breeding aims to maximize genetic variances rather than genetic gains, such a rotational breeding program might be a valuable option. However, willingness of farmers to adopt such a breeding program needs to be investigated because the rotational use of village bulls among villages within groups is not a customary practice in the Butana region, and it increases the organizational complexity.

Genetic improvement in dairy cattle is largely determined by the merit of bulls used as sires of each generation; therefore, dairy bulls selection is an important step in any cattle breeding program (Andrabi and Moran, 2007; Kariuki et al., 2014). Breeders rely on various selection methods to improve breeding goal traits. In this study, random selection, phenotypic selection, and selection of young bulls based on their EBV were simulated. We found that a substantial genetic gain could be achieved by selection based on EBV of young bulls in all breeding scenarios. In addition, a higher genetic variance was obtained by selection based on EBV in the simulated breeding scenarios. This may indicate that the effect of selection on reducing the additive genetic variance (i.e., change of allele frequencies) was small. Several studies have shown selection based on EBV to achieve better genetic improvement. For instance, in their work on developing breeding schemes for pasture-based dairy production systems in Kenya, Kahi et al. (2004) demonstrated that in a well-organized open-nucleus breeding program, young bull selection would be profitable and result in overall improvement of production in dairy cattle. Syrstad and Ruane (1998)

compared 2 traditional schemes for dairy bull selection in the tropics, namely young bull selection (i.e., selection based on bulls' dams' performances and selection based on bulls' daughters' performances; progeny testing). The authors found that young bull selection gave faster genetic gain per year due to a shorter generation interval. Philipsson et al. (2011) also emphasized that selection based on EBV of young bulls would be a better option than engaging in a poorly organized dairy cattle progeny testing program because selection based on progeny testing prolongs the generation interval, contributing to slower genetic progress. Additionally, a young bull selection scheme is practically simple and less expensive (Zumbach and Peters, 2002), which makes it suitable to animal breeding programs in the tropics. In Sudan, the selection of young bulls based on bulls' dams' milk yield performances is a customary practice by Butana cattle owners (Musa et al., 2006; Mohammed et al., 2014; Omer et al., 2020), and should thus be enhanced for the future genetic improvement of this breed. However, phenotypic selection yielded lower genetic gain compared with selection based on EBV. According to Oldenbroek and van der Waaij (2015), phenotypic selection is a straightforward way of ranking animals as breeding candidates, but it is not always the most accurate way if the phenotype is not available for all animals, such as for milk production of males. However, it could be used for screening farmers' herds for selecting outstanding bulls or cows to initiate a base population for a breeding program (Philipsson et al., 2011). Organized recording schemes using all available information about relatives (i.e., maternal and paternal half-sisters of sires and dams) could form the basis for breeding value estimation, further enhancing the genetic progress of a future breeding program for Butana cattle in Sudan.

For a successful implementation of selection based on EBV for Butana cattle improvement, recording schemes should be established, and performance recordings should be done in each farm within a cooperative group. In this regard, the main strength reported in the previous work (Omer et al., 2020) was that Butana cattle farmers were willing to adopt performance record keeping. However, motivating farmers by offering incentives such as discounts on breeding males, veterinary health care, vaccinations, exhibitions, and access to market auctions, sales, and other production inputs could positively affect successful adoption of record keeping (Kahi et al., 2005; Mueller et al., 2015; Zoma-Traoré et al., 2021). The strong link and collaborations among farmers, relevant livestock development institutions (e.g., universities and research stations), and other development partners are widely suggested in developing

countries to ensure information sharing (Wurzinger et al., 2011; Ibeagha-Awemu et al., 2019) and to help cooperative farmers receive essential inputs (e.g., measuring and recording facilities), genetic evaluation software, and training to support genetic improvement activities (Kahi et al., 2005; Kosgey and Okeyo, 2007). Mueller et al. (2015) analyzed 8 community-based breeding programs located in countries of Latin America, Africa, and Asia, and concluded that the involvement of relevant institutions in the planning and implementation of breeding stages is most important for the success of farmer cooperative breeding programs.

CONCLUSIONS

In the present study, we simulated 3 alternative breeding scenarios for the genetic improvement of the milk yield of Butana cattle under smallholder producers' production conditions in Sudan using different selection methods. Our results showed the highest genetic gain for the village bull breeding scenario. Also, the genetic gain was highest with selection based on EBV for each breeding scenario. Conspicuously, the genetic variance was most strongly maintained for the rotational use of village bulls within village groups. Genetic gains under random selection across all breeding programs were much lower, and genetic variances were also often smaller than for phenotypic selection and selection based on EBV. Thus, this breeding program may have no relevance for future breed development of Butana cattle. The findings of the present study will assist in designing a practical breed improvement program for Butana cattle kept under smallholder production conditions in Sudan. They may also serve as a blueprint for the development of breeding programs for other local breeds kept under similar conditions in the country.

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